

Figure 1. Sequence of *C. pneumoniae* OMP (outer membrane protein) gene.

5 gtggcttgat tttgaaaaag gtccatggat gtgtttataa tgttcaaggt ctccctatcc 60  
aaacattgaa atacttgcta gaggagttga acatcgatct atg gga cta ttc cat 115  
Met Gly Leu Phe His  
1 5

10 cta act ctc ttt gga ctt tta ttg tgt agt ctt ccc att tct ctt gtt 163  
Leu Thr Leu Phe Gly Leu Leu Leu Cys Ser Leu Pro Ile Ser Leu Val  
10 15 20

15 gct aaa ttc cct gag tct gta ggt cat aag atc ctt tat ata agt acg 211  
Ala Lys Phe Pro Glu Ser Val Gly His Lys Ile Leu Tyr Ile Ser Thr  
25 30 35

20 caa tct aca cag cag gcc tta gca aca tat ctg gaa gct cta gat gcc 259  
Gln Ser Thr Gln Gln Ala Leu Ala Thr Tyr Leu Glu Ala Leu Asp Ala  
40 45 50

25 tac ggt gat cat gac ttc ttc gtt tta aga aaa atc gga gaa gac tat 307  
Tyr Gly Asp His Asp Phe Phe Val Leu Arg Lys Ile Gly Glu Asp Tyr  
55 60 65

30 ctc aag caa agc atc cac tcc tca gat ccg caa act aga aaa agc acc 355  
Leu Lys Gln Ser Ile His Ser Ser Asp Pro Gln Thr Arg Lys Ser Thr  
70 75 80 85

35 atc att gga gca ggc ctg gcg gga tct tca gaa gcc ttg gac gtg ctc 403  
Ile Ile Gly Ala Gly Leu Ala Gly Ser Ser Glu Ala Leu Asp Val Leu  
90 95 100

40 tcc caa gct atg gaa act gca gac ccc ctg cag cag cta ctg gtt tta 451  
Ser Gln Ala Met Glu Thr Ala Asp Pro Leu Gln Gln Leu Leu Val Leu  
105 110 115

45 tcg gca gtc tca gga cat ctt ggg aaa act tct gac gac tta ctg ttt 499  
Ser Ala Val Ser Gly His Leu Gly Lys Thr Ser Asp Asp Leu Leu Phe  
120 125 130

50 aaa gct tta gca tct ccc tat cct gtc atc cgc tta gaa gcc gcc tat 547  
Lys Ala Leu Ala Ser Pro Tyr Pro Val Ile Arg Leu Glu Ala Ala Tyr  
135 140 145

55 aga ctt gct aat ttg aag aac act aaa gtc att gat cat cta cat tct 595  
Arg Leu Ala Asn Leu Lys Asn Thr Lys Val Ile Asp His Leu His Ser  
150 155 160 165

60 ttc att cat aag ctt ccc gaa gaa atc caa tgc cta tct gcg gca ata 643  
Phe Ile His Lys Leu Pro Glu Glu Ile Gln Cys Leu Ser Ala Ala Ile  
170 175 180

55 ttc cta cgc ttg gag act gaa gaa tct gat gct tat att cgg gat ctc 691  
Phe Leu Arg Leu Glu Thr Glu Glu Ser Asp Ala Tyr Ile Arg Asp Leu  
185 190 195

60 tta gct gcc aag aaa agc gcg att cgg agt gcc aca gct ttg cag atc 739  
Leu Ala Ala Lys Lys Ser Ala Ile Arg Ser Ala Thr Ala Leu Gln Ile  
200 205 210

03662416-091300

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gga gaa tac caa caa aaa cgc ttt ctt ccg aca ctt agg aat ttg cta 787  
Gly Glu Tyr Gln Gln Lys Arg Phe Leu Pro Thr Leu Arg Asn Leu Leu  
215 220 225

5    acg agt gcg tct cct caa gat caa gaa gct att ctt tat gct tta ggg      835  
     Thr Ser Ala Ser Pro Gln Asp Gln Glu Ala Ile Leu Tyr Ala Leu Gly  
     230                          235                          240                          245

10    aag ctt aag gat ggt cag agc tac tac aat ata aaa aag caa ttg cag    883  
     Lys Leu Lys Asp Gly Gln Ser Tyr Tyr Asn Ile Lys Lys Gln Leu Gln  
                250                            255                            260

aag cct gat gtg gat gtc act tta gca gca gct caa gct tta att gct      931  
Lys Pro Asp Val Asp Val Thr Leu Ala Ala Ala Gln Ala Leu Ile Ala

15                          265                          270                          275

ttg ggg aaa gaa gag gac gct ctt ccc gtg ata aaa aag caa gca ctt 979  
Leu Gly Lys Glu Glu Asp Ala Leu Pro Val Ile Lys Lys Gln Ala Leu  
280 285 290

gag gag cgg cct cga gcc ctg tat gcc tta cgg cat cta ccc tct gag 1027  
Glu Glu Arg Pro Arg Ala Leu Tyr Ala Leu Arg His Leu Pro Ser Glu  
295 300 305

25    ata ggg att ccg att gcc ctg ccg ata ttc cta aaa act aag aac agc      1075  
      Ile Gly Ile Pro Ile Ala Leu Pro Ile Phe Leu Lys Thr Lys Asn Ser  
      310                          315                          320                          325

30    gaa gcc aag ttg aat gta gct tta gct ctc tta gag tta ggg tgt gac    1123  
     Glu Ala Lys Leu Asn Val Ala Leu Ala Leu Leu Glu Leu Gly Cys Asp  
                330                      335                      340

acc cct aaa cta ctg gaa tac att acc gaa agg ctt gtc caa cca cat 1171  
Thr Pro Lys Leu Leu Glu Tyr Ile Thr Glu Arg Leu Val Gln Pro His  
35 345 350 355

tat	aat	gag	act	cta	gcc	ttg	agt	ttc	tct	aag	ggg	cgt	act	tta	caa	1219
Tyr	Asn	Glu	Thr	Leu	Ala	Leu	Ser	Phe	Ser	Lys	Gly	Arg	Thr	Leu	Gln	
		360					365					370				

aat tgg aag cgg gtg aac atc ata gtc cct caa gat ccc cag gag agg 1267  
Asn Trp Lys Arg Val Asn Ile Ile Val Pro Gln Asp Pro Gln Glu Arg  
375 380 385

45    gaa agg ttg ctc tcc aca acc cga ggt ctt gaa gag cag atc ctt acg      1315  
      Glu Arg Leu Leu Ser Thr Thr Arg Gly Leu Glu Glu Gln Ile Leu Thr  
      390                          395                          400                          405

50    ttt ctc ttc cgc cta cct aaa gaa gct tac ctc ccc tgt att tat aag    1363  
     Phe Leu Phe Arg Leu Pro Lys Glu Ala Tyr Leu Pro Cys Ile Tyr Lys  
                410                            415                            420

ctt ttg gcg agt cag aaa act cag ctt gcc act act gcg att tct ttt 1411  
Leu Leu Ala Ser Gln Lys Thr Gln Leu Ala Thr Thr Ala Ile Ser Phe

55                   425                         430                             435

tta	agt	cac	acc	tca	cat	cag	gaa	gcc	tta	gat	cta	ctt	ttc	caa	gct	1459
Leu	Ser	His	Thr	Ser	His	Gln	Glu	Ala	Leu	Asp	Leu	Leu	Phe	Gln	Ala	
		440					445					450				

gcg aag ctt cct gga gaa cct atc atc cgc gcc tat gca gat ctt gct 1507  
Ala Lys Leu Pro Gly Glu Pro Ile Ile Arg Ala Tyr Ala Asp Leu Ala  
455 460 465

[illegible]

att tat aat ctc acc aaa gat cct gaa aaa aaa cgt tct ctc cat gat 1555  
Ile Tyr Asn Leu Thr Lys Asp Pro Glu Lys Lys Arg Ser Leu His Asp  
470 475 480 485

5    tat gca aaa aag cta att cag gaa acc ttg tta ttt gtg gac acg gaa    1603  
Tyr Ala Lys Lys Leu Ile Gln Glu Thr Leu Leu Phe Val Asp Thr Glu  
                    490                    495                    500

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10      aac caa aga ccc cat ccc agc atg ccc tat cta cgt tat cag gtc acc 1651
      Asn Gln Arg Pro His Pro Ser Met Pro Tyr Leu Arg Tyr Gln Val Thr
              505                      510                      515

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cca gaa agc cgt acg aag ctc atg ttg gat att cta gag aca cta gcc 1699  
Pro Glu Ser Arg Thr Lys Leu Met Leu Asp Ile Leu Glu Thr Leu Ala  
15 520 525 530

acc tcg aag tct tcc gaa gat atc cgt tta ttg ata caa ctg atg acg 1747  
Thr Ser Lys Ser Ser Glu Asp Ile Arg Leu Leu Ile Gln Leu Met Thr  
535 540 545

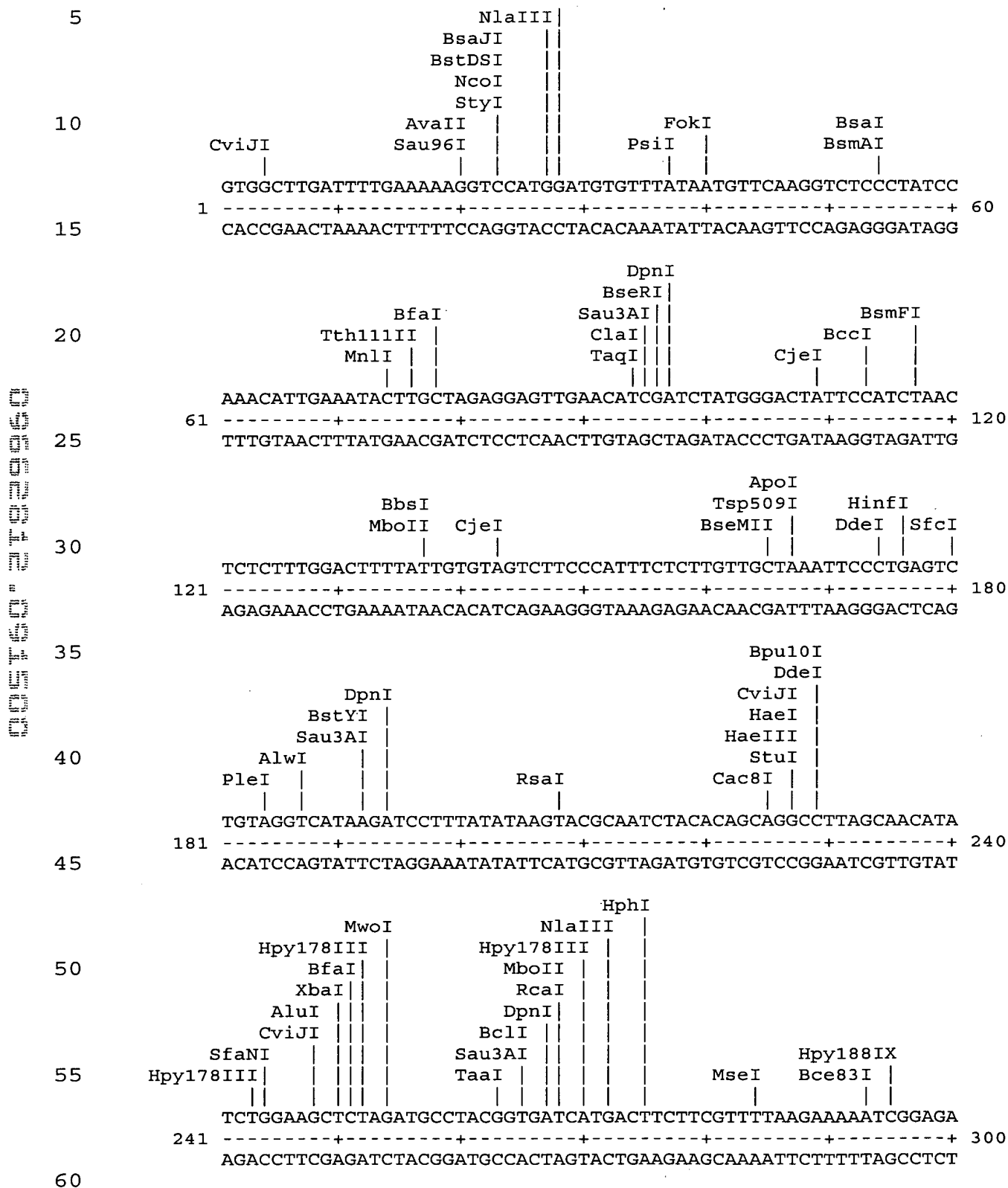
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Glu Gly Asp Ala Lys Asn Phe Pro Val Leu Ala Gly Leu Leu Ile Lys  
550 555 560 565

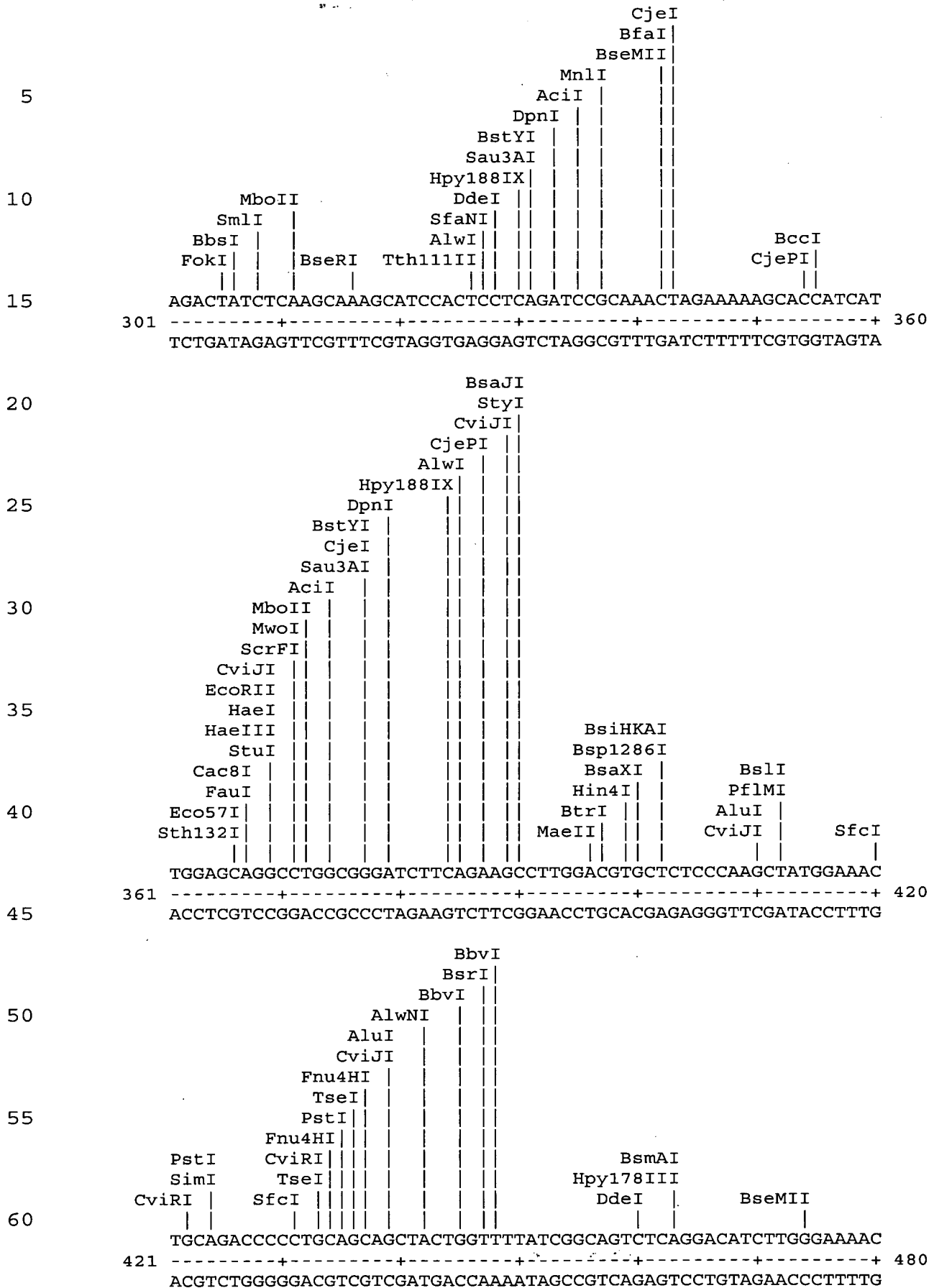
25 att gtg gag taacccaac ctacgtctta tgaaacgttg cttcttattt 1844  
Ile Val Glu

ctagcttcct ttgttcttat gggttcctca gctgatgctt tgactcatca agaggctgtg 1904

30    aaa    1907

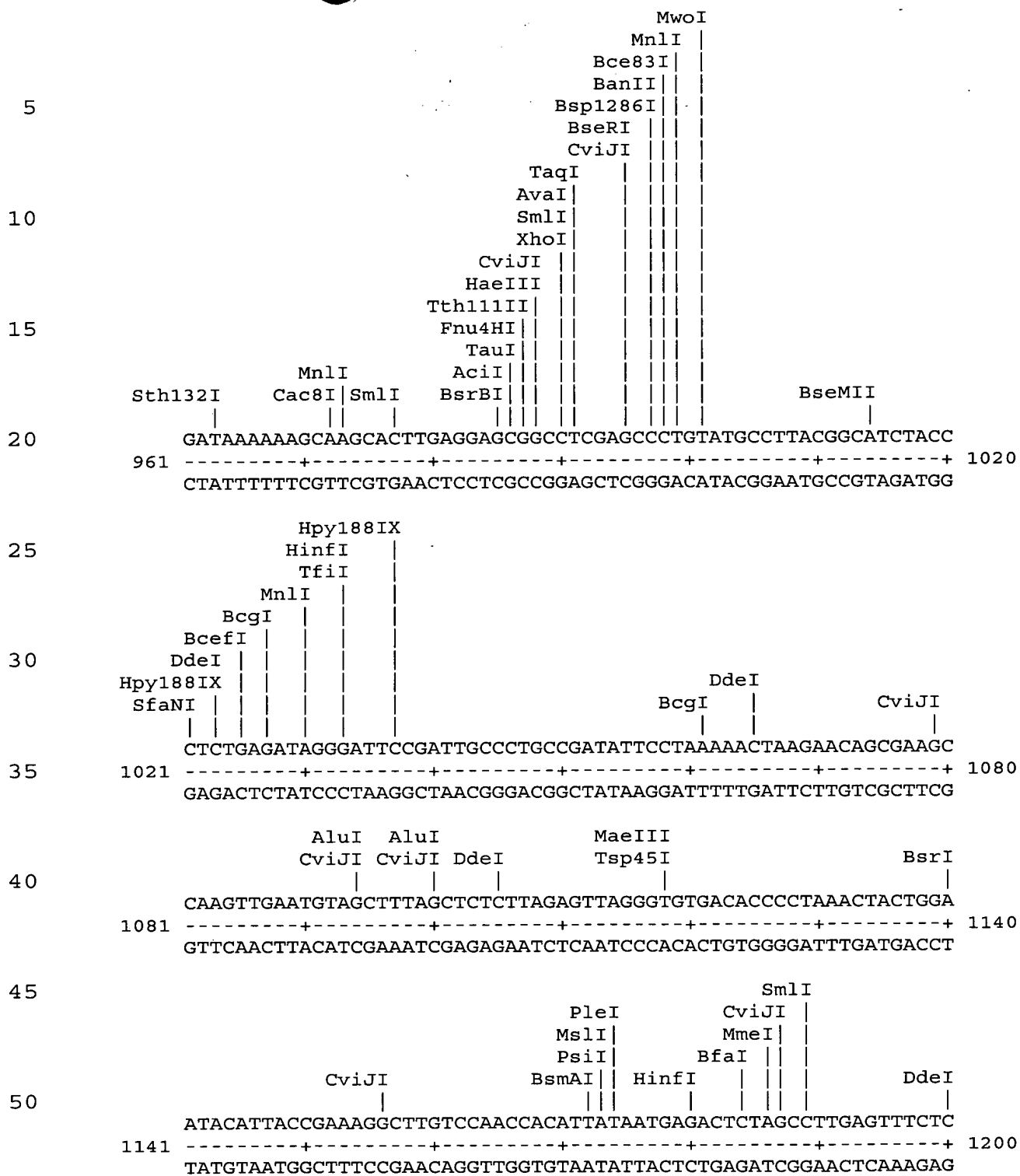
Figure 2. Restriction enzyme analysis of the *C. pneumoniae* OMP (outer membrane protein) gene.





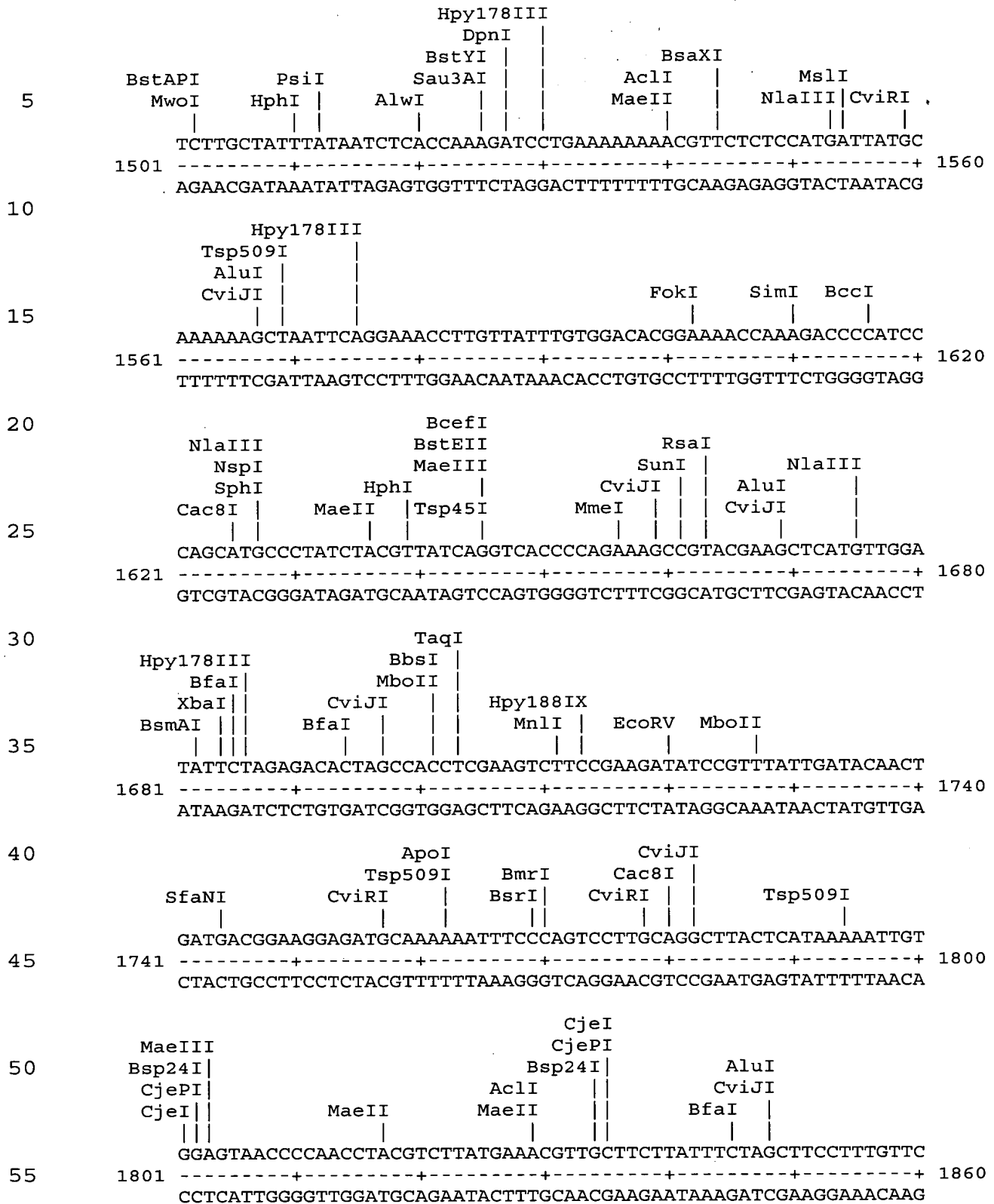
50

960









[illegible]

Figure 4: Protective efficacy of DNA immunization with pCAmg002.

